

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Farmaceutisk Laboratorium Ferring A/S
- (B) STREET: Indertoften 10
- (C) CITY: Vanloese
- (E) COUNTRY: Denmark
- (F) POSTAL CODE (ZIP): DK-2720

(ii) TITLE OF INVENTION: Modified human TNF-alpha molecules, DNA encoding them, and vaccines containing said modified TNF-alpha or DNA

(iii) NUMBER OF SEQUENCES: 42

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /codon_start= 1
/function= "Antigen"
/product= "TNF-alpha analog"
/evidence= EXPERIMENTAL
/gene= "tnf2-1"
/standard_name= "TNF2-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT CAG TAC ATT AAA GCC AAT 48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Gln Tyr Ile Lys Ala Asn
1 5 10 15

TCT AAA TTC ATC GGT ATA ACT GAG CTG CAG CTC CAG TGG CTG AAC CGC 96
Ser Lys Phe Ile Gly Ile Thr Glu Leu Gln Leu Gln Trp Leu Asn Arg
20 25 30

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CGG	GCC	AAT	GCC	CTC	CTG	GCC	AAT	GGC	GTG	GAG	CTG	AGA	GAT	AAC	CAG	144
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	
		35					40					45				
CTG	GTG	GTG	CCA	TCA	GAG	GGC	CTG	TAC	CTC	ATC	TAC	TCC	CAG	GTC	CTC	192
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	
	50					55					60					
TTC	AAG	GGC	CAA	GGC	TGC	CCC	TCC	ACC	CAT	GTG	CTC	CTC	ACC	CAC	ACC	240
Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	
65					70					75					80	
ATC	AGC	CGC	ATC	GCC	GTC	TCC	TAC	CAG	ACC	AAG	GTC	AAC	CTC	CTC	TCT	288
Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	
				85				90						95		
GCC	ATC	AAG	AGC	CCC	TGC	CAG	AGG	GAG	ACC	CCA	GAG	GGG	GCT	GAG	GCC	336
Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	
			100					105					110			
AAG	CCC	TGG	TAT	GAG	CCC	ATC	TAT	CTG	GGA	GGG	GTC	TTC	CAG	CTG	GAG	384
Lys	Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	
	115					120						125				
AAG	GGT	GAC	CGA	CTC	AGC	GCT	GAG	ATC	AAT	CGG	CCC	GAC	TAT	CTC	GAC	432
Lys	Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	
	130					135					140					
TTT	GCC	GAG	TCT	GGG	CAG	GTC	TAC	TTT	GGG	ATC	ATT	GCC	CTC	TAG		477
Phe	Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu	*		
145					150					155						

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Gln	Tyr	Ile	Lys	Ala	Asn	
1				5					10					15		
Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Leu	Gln	Leu	Gln	Trp	Leu	Asn	Arg	
		20						25					30			
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	
		35					40					45				
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	
	50					55					60					
Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	
65					70					75					80	
Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	
				85					90					95		

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Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
 100 105 110

Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
 115 120 125

Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
 130 135 140

Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: /codon_start= 1
 /function= "Antigen"
 /product= "TNF-alpha analog"
 /gene= "tnfP2-3"
 /standard_name= "TNF2-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
160 165 170 175	
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
195 200 205	
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
210 215 220	
TTC CAG TAC ATA AAG GCC AAC TCC AAG TTT ATC GGC ATC ACC GAG CTC	240
Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu	
225 230 235	

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(2) INFORMATION FOR SEQ ID NO: 4:

(A) LENGTH: 159 amino acids

TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met 1	Val	Arg	Ser	Ser 5	Ser	Arg	Thr	Pro	Ser 10	Asp	Lys	Pro	Val	Ala 15	His
Val	Val	Ala	Asn 20	Pro	Gln	Ala	Glu	Gly 25	Gln	Leu	Gln	Trp	Leu 30	Asn	Arg
Arg	Ala	Asn 35	Ala	Leu	Leu	Ala	Asn 40	Gly	Val	Glu	Leu	Arg 45	Asp	Asn	Gln
Leu	Val 50	Val	Pro	Ser	Glu	Gly 55	Leu	Tyr	Leu	Ile	Tyr 60	Ser	Gln	Val	Leu
Phe 65	Gln	Tyr	Ile	Lys	Ala 70	Asn	Ser	Lys	Phe	Ile 75	Gly	Ile	Thr	Glu	Leu 80
Ile	Ser	Arg	Ile	Ala 85	Val	Ser	Tyr	Gln	Thr 90	Lys	Val	Asn	Leu	Leu 95	Ser
Ala	Ile	Lys	Ser 100	Pro	Cys	Gln	Arg	Glu	Thr 105	Pro	Glu	Gly	Ala 110	Glu	Ala
Lys	Pro	Trp 115	Tyr	Glu	Pro	Ile	Tyr 120	Leu	Gly	Gly	Val	Phe 125	Gln	Leu	Glu
Lys	Gly 130	Asp	Arg	Leu	Ser	Ala 135	Glu	Ile	Asn	Arg	Pro 140	Asp	Tyr	Leu	Asp
Phe 145	Ala	Glu	Ser	Gly	Gln 150	Val	Tyr	Phe	Gly	Ile 155	Ile	Ala	Leu	*	

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: /codon_start= 1
/function= "Antigen"
/product= "TNF-alpha analog"
/gene= "tnfP2-4"
/standard_name= "TNF2-4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
160 165 170 175	
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
195 200 205	
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
210 215 220	
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC	240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
225 230 235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT	288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
240 245 250 255	
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
260 265 270	
AAG CCC CAG TAT ATC AAG GCC AAT TCG AAA TTC ATC GGC ATC ACG GAG	384
Lys Pro Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu	
275 280 285	
CTC GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Leu Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
290 295 300	

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TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG
 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *
 305 310 315

477

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
 1 5 10 15
 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
 20 25 30
 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
 35 40 45
 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
 50 55 60
 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
 65 70 75 80
 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
 85 90 95
 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
 100 105 110
 Lys Pro Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
 115 120 125
 Leu Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
 130 135 140
 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

09060294.041598

(A) ORGANISM: Homo sapiens

(A) NAME/KEY: CDS

(D) OTHER INFORMATION: /function= "Antigen"

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/product= "TNF-alpha analog"
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/gene= "tnfP2-5"
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/standard name= "TNF2-5"
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ATG Met 160	GTC Val	AGA Arg	TCA Ser	TCT Ser	TCT Ser 165	CGA Arg	ACC Thr	CCG Pro	AGT Ser	GAC Asp 170	AAG Lys	CCT Pro	GTA Val	GCC Ala	CAT His 175	48
GTT Val	GTA Val	GCA Ala	AAC Asn	CCT Pro 180	CAA Gln	GCT Ala	GAG Glu	GGG Gly	CAG Gln 185	CTC Leu	CAG Gln	TGG Trp	CTG Leu	AAC Asn 190	CGC Arg	96
CGG Arg	GCC Ala	AAT Asn	GCC Ala 195	CTC Leu	CTG Leu	GCC Ala	AAT Asn	GGC Gly 200	GTG Val	GAG Glu	CTG Leu	AGA Arg	GAT Asp 205	AAC Asn	CAG Gln	144
CTG Leu	GTG Val	GTG Val 210	CCA Pro	TCA Ser	GAG Glu	GGC Gly	CTG Leu 215	TAC Tyr	CTC Leu	ATC Ile	TAC Tyr	TCC Ser 220	CAG Gln	GTC Val	CTC Leu	192
TTC Phe	AAG Lys 225	GGC Gly	CAA Gln	GGC Gly	TGC Cys	CCC Pro 230	TCC Ser	ACC Thr	CAT His	GTG Val	CTC Leu 235	CTC Leu	ACC Thr	CAC His	ACC Thr	240
ATC Ile 240	AGC Ser	CGC Arg	ATC Ile	GCC Ala	GTC Val 245	TCC Ser	TAC Tyr	CAG Gln	ACC Thr	AAG Lys 250	GTC Val	AAC Asn	CTC Leu	CTC Leu	TCT Ser 255	288
GCC Ala	ATC Ile	AAG Lys	AGC Ser	CCC Pro 260	TGC Cys	CAG Gln	AGG Arg	GAG Glu	ACC Thr 265	CCA Pro	GAG Glu	GGG Gly	GCT Ala	GAG Glu 270	GCC Ala	336
AAG Lys	CCC Pro	TGG Trp	TAT Tyr 275	GAG Glu	CCC Pro	ATC Ile	TAT Tyr	CTG Leu 280	GGA Gly	GGG Gly	GTC Val	TTC Phe	CAG Gln 285	CTG Leu	GAG Glu	384
AAG Lys	GGT Gly	GAC Asp 290	CGA Arg	CAG Gln	TAC Tyr	ATT Ile	AAG Lys 295	GCC Ala	AAT Asn	TCG Ser	AAG Lys	TTC Phe 300	ATT Ile	GGC Gly	ATC Ile	432
ACT Thr	GAG Glu 305	CTG Leu	TCT Ser	GGG Gly	CAG Gln	GTC Val 310	TAC Tyr	TTT Phe	GGG Gly	ATC Ile	ATT Ile 315	GCC Ala	CTC Leu	TAG *		477

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His
1				5					10					15	
Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg
			20					25					30		
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln
		35					40					45			
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu
	50					55					60				
Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr
65					70					75					80
Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser
				85					90					95	
Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala
			100					105					110		
Lys	Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu
		115					120					125			
Lys	Gly	Asp	Arg	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile
	130					135					140				
Thr	Glu	Leu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu	*	
145					150					155					

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION:1..477
      (D) OTHER INFORMATION:/codon_start= 1
          /function= "Antigen"
          /product= "TNF-alpha analog"
          /gene= "tnfp2-7"
          /standard name= "TNF2-7"
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ATG Met 160	GTC Val	AGA Arg	TCA Ser	TCT Ser	TCT Ser 165	CGA Arg	ACC Thr	CCG Pro	AGT Ser	GAC Asp 170	AAG Lys	CCT Pro	GTA Val	GCC Ala	CAT His 175	48
GTT Val	GTA Val	GCA Ala	AAC Asn	CCT Pro 180	CAA Gln	GCT Ala	GAG Glu	GGG Gly	CAG Gln 185	CTC Leu	CAG Gln	TGG Trp	CTG Leu	AAC Asn 190	CGC Arg	96
CGG Arg	GCC Ala	AAT Asn	GCC Ala 195	CTC Leu	CTG Leu	GCC Ala	AAT Asn	GGC Gly 200	GTG Val	GAG Glu	CTG Leu	AGA Arg	GAT Asp 205	AAC Asn	CAG Gln	144
CTG Leu	GTG Val	GTG Val 210	CCA Pro	TCA Ser	GAG Glu	GGC Gly	CTG Leu 215	TAC Tyr	CTC Leu	ATC Ile	TAC Tyr	TCC Ser 220	CAG Gln	GTC Val	CTC Leu	192
TTC Phe	AAG Lys 225	GGC Gly	CAA Gln	GGC Gly	TGC Cys	CCC Pro 230	TCC Ser	ACC Thr	CAT His	GTG Val	CTC Leu 235	CAG Gln	TAC Tyr	ATC Ile	AAA Lys	240
GCT Ala 240	AAC Asn	TCC Ser	AAA Lys	TTC Phe	ATC Ile 245	GGC Gly	ATC Ile	ACC Thr	GAA Glu	CTG Leu 250	GTT Val	AAC Asn	CTC Leu	CTC Leu	TCT Ser 255	288
GCC Ala	ATC Ile	AAG Lys	AGC Ser	CCC Pro 260	TGC Cys	CAG Gln	AGG Arg	GAG Glu	ACC Thr 265	CCA Pro	GAG Glu	GGG Gly	GCT Ala	GAG Glu 270	GCC Ala	336
AAG Lys	CCC Pro	TGG Trp	TAT Tyr 275	GAG Glu	CCC Pro	ATC Ile	TAT Tyr	CTG Leu 280	GGA Gly	GGG Gly	GTC Val	TTC Phe	CAG Gln 285	CTG Leu	GAG Glu	384
AAG Lys	GGT Gly	GAC Asp 290	CGA Arg	CTC Leu	AGC Ser	GCT Ala	GAG Glu 295	ATC Ile	AAT Asn	CGG Arg	CCC Pro 300	GAC Asp	TAT Tyr	CTC Leu	GAC Asp	432
TTT Phe	GCC Ala 305	GAG Glu	TCT Ser	GGG Gly	CAG Gln	GTC Val 310	TAC Tyr	TTT Phe	GGG Gly	ATC Ile	ATT Ile 315	GCC Ala	CTC Leu	TAG *		477

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His
1				5					10					15	
Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg
			20					25					30		
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln
		35					40					45			

Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
 50 55 60
 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Gln Tyr Ile Lys
 65 70 75 80
 Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Val Asn Leu Leu Ser
 85 90 95
 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
 100 105 110
 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
 115 120 125
 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
 130 135 140
 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: /codon_start= 1
 /function= "Antigen"
 /product= "TNF-alpha analog"
 /gene= "tnfP30-1"
 /standard_name= "TNF30-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT TTC AAC AAT TTT ACC GTA	48
Met Val Arg Ser Ser Arg Thr Pro Ser Phe Asn Asn Phe Thr Val	
160 165 170 175	
AGC TTT TGG CTC CGT GTA CCT AAG GTG TCG GCC TCG CAC CTG GAG CGC	96
Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
195 200 205	

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CTG	GTG	GTG	CCA	TCA	GAG	GGC	CTG	TAC	CTC	ATC	TAC	TCC	CAG	GTC	CTC	192
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	
		210					215					220				
TTC	AAG	GGC	CAA	GGC	TGC	CCC	TCC	ACC	CAT	GTG	CTC	CTC	ACC	CAC	ACC	240
Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	
	225					230					235					
ATC	AGC	CGC	ATC	GCC	GTC	TCC	TAC	CAG	ACC	AAG	GTC	AAC	CTC	CTC	TCT	288
Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	
240					245					250					255	
GCC	ATC	AAG	AGC	CCC	TGC	CAG	AGG	GAG	ACC	CCA	GAG	GGG	GCT	GAG	GCC	336
Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	
				260					265					270		
AAG	CCC	TGG	TAT	GAG	CCC	ATC	TAT	CTG	GGA	GGG	GTC	TTC	CAG	CTG	GAG	384
Lys	Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	
			275					280					285			
AAG	GGT	GAC	CGA	CTC	AGC	GCT	GAG	ATC	AAT	CGG	CCC	GAC	TAT	CTC	GAC	432
Lys	Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	
		290					295					300				
TTT	GCC	GAG	TCT	GGG	CAG	GTC	TAC	TTT	GGG	ATC	ATT	GCC	CTC	TAG		477
Phe	Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu	*		
	305					310					315					

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Phe	Asn	Asn	Phe	Thr	Val	
1				5					10					15		
Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Arg	
		20					25						30			
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	
		35					40					45				
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	
	50					55					60					
Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	
65				70						75				80		
Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	
			85					90					95			
Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	
			100					105					110			
Lys	Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	
	115						120					125				

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Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
130 135 140

Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *
145 150 155

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..477
- (D) OTHER INFORMATION:/codon_start= 1
/function= "Antigen"
/product= "TNF-alpha analog"
/gene= "tnfP30-2"
/standard_name= "TNF30-2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
160 165 170 175	
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT TTC AAC AAC TTC ACA GTT AGC TTC	144
Arg Ala Asn Ala Leu Leu Ala Asn Phe Asn Asn Phe Thr Val Ser Phe	
195 200 205	
TGG TTG AGG GTA CCA AAG GTC TCG GCC AGC CAC CTC GAG CAG GTC CTC	192
Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Val Leu	
210 215 220	
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC	240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
225 230 235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT	288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
240 245 250 255	
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
260 265 270	

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AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
275 280 285	
AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
290 295 300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG	477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
305 310 315	

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
1 5 10 15	
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
20 25 30	
Arg Ala Asn Ala Leu Leu Ala Asn Phe Asn Asn Phe Thr Val Ser Phe	
35 40 45	
Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Val Leu	
50 55 60	
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
65 70 75 80	
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
85 90 95	
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
100 105 110	
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
115 120 125	
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
130 135 140	
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
145 150 155	

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..477
(D) OTHER INFORMATION: /codon_start= 1
/function= "Antigen"
/product= "TNF-alpha analog"
/gene= "tnfP30-3"
/standard_name= "TNF30-3"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
160 165 170 175	
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
195 200 205	
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
210 215 220	
TTC AAC AAC TTT ACC GTC TCC TTC TGG CTT CGG GTA CCC AAG GTC AGC	240
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser	
225 230 235	
GCT AGC CAC CTC GAG GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT	288
Ala Ser His Leu Glu Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
240 245 250 255	
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
260 265 270	
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
275 280 285	
AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
290 295 300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG	477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
305 310 315	

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(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
 1 5 10 15
 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
 20 25 30
 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
 35 40 45
 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
 50 55 60
 Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
 65 70 75 80
 Ala Ser His Leu Glu Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
 85 90 95
 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
 100 105 110
 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
 115 120 125
 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
 130 135 140
 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:1..477

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(D) OTHER INFORMATION:/function= "Antigen"
 /product= "TNF-alpha analog"
 /gene= "tnfp30-4"
 /standard_name= "TNF30-4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATG	GTC	AGA	TCA	TCT	TCT	CGA	ACC	CCG	AGT	GAC	AAG	CCT	GTA	GCC	CAT	48
Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His	
160						165				170					175	
GTT	GTA	GCA	AAC	CCT	CAA	GCT	GAG	GGG	CAG	CTC	CAG	TGG	CTG	AAC	CGC	96
Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	
				180					185					190		
CGG	GCC	AAT	GCC	CTC	CTG	GCC	AAT	GGC	GTG	GAG	CTG	AGA	GAT	AAC	CAG	144
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	
			195					200					205			
CTG	GTG	GTG	CCA	TCA	GAG	GGC	CTG	TAC	CTC	ATC	TAC	TCC	CAG	GTC	CTC	192
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	
		210					215					220				
TTC	AAG	GGC	CAA	GGC	TGC	CCC	TCC	ACC	CAT	GTG	CTC	CTC	ACC	CAC	ACC	240
Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	
	225				230						235					
ATC	AGC	CGC	ATC	GCC	GTC	TCC	TAC	CAG	ACC	AAG	GTC	AAC	CTC	CTC	TCT	288
Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	
					245					250					255	
GCC	ATC	AAG	AGC	CCC	TGC	CAG	AGG	GAG	ACC	CCA	TTT	AAT	AAT	TTC	ACC	336
Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Phe	Asn	Asn	Phe	Thr	
				260					265					270		
GTG	TCC	TTC	TGG	TTG	CGC	GTC	CCT	AAG	GTA	AGC	GCT	TCC	CAC	CTG	GAG	384
Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	
			275					280					285			
AAG	GGT	GAC	CGA	CTC	AGC	GCT	GAG	ATC	AAT	CGG	CCC	GAC	TAT	CTC	GAC	432
Lys	Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	
		290					295					300				
TTT	GCC	GAG	TCT	GGG	CAG	GTC	TAC	TTT	GGG	ATC	ATT	GCC	CTC	TAG		477
Phe	Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu	*		
	305					310					315					

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His
1				5					10					15	

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Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
 20 25 30
 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
 35 40 45
 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
 50 55 60
 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
 65 70 75 80
 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
 85 90 95
 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Phe Asn Asn Phe Thr
 100 105 110
 Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu
 115 120 125
 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
 130 135 140
 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: /codon_start= 1
 /function= "Antigen"
 /product= "TNF-alpha analog"
 /gene= "tnfp30-5"
 /standard_name= "TNF30-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Lys Pro Val Ala His	
160 165 170 175	
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
180 185 190	

CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
195 200 205	
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
210 215 220	
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC	240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
225 230 235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT	288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
240 245 250 255	
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
260 265 270	
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
275 280 285	
AAG GGT GAC CGA TTC AAC AAT TTC ACC GTA AGC TTC TGG CTT CGC GTC	432
Lys Gly Asp Arg Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val	
290 295 300	
CCT AAG GTG TCT GCG TCG CAC CTC GAA GGG ATC ATT GCC CTC TAG	477
Pro Lys Val Ser Ala Ser His Leu Glu Gly Ile Ile Ala Leu *	
305 310 315	

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
1 5 10 15	
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
20 25 30	
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
35 40 45	
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
50 55 60	
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
65 70 75 80	
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
85 90 95	

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Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
 100 105 110

Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
 115 120 125

Lys Gly Asp Arg Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val
 130 135 140

Pro Lys Val Ser Ala Ser His Leu Glu Gly Ile Ile Ala Leu *
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..24
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION: /function= "Primer for PCR cloning
 of DNA encoding TNF-alpha"
 /product= "Primer binding to TNF-alpha gene"
 /evidence= EXPERIMENTAL
 /standard_name= "TNF-alpha Primer I"
 /label= Primer1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GACAAGCCCA TGGTCAGATC ATCT

24

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..30
 - (C) IDENTIFICATION METHOD: experimental

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(D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha"
/product= "Primer binding to TNF-alpha gene"
/evidence= EXPERIMENTAL
/standard_name= "TNF-alpha Primer II"
/label= Primer2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TCTCTAGAGG GCAATGATCC CAAAGTAGAC

30

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:1..21
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha"
/product= "Primer binding to TNF-alpha gene"
/evidence= EXPERIMENTAL
/standard_name= "TNF-alpha Primer III"
/label= Primer3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CCCAAAGTAG ACCTGCCCAG A

21

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: insertion_seq
(B) LOCATION:7..51
(C) IDENTIFICATION METHOD: experimental

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(D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut2-1""
/label= mut2-1
/note= "Primer "mut2-1" is a synthetically synthesised
69-mer oligonucleotide comprising DNA encoding the human
T cell epitope P2 between stretches of DNA homologous to
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ACCCCGAGTC AGTACATTAA AGCCAATTCT AAATTCATCG GTATAACTGA GCTGCAGCTC 60
CAGTGGCTG 69

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:
(A) NAME/KEY: insertion_seq
(B) LOCATION:15..59
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut2-3""
/label= mut2-3
/note= "Primer "mut2-3" is a synthetically synthesised
73-mer oligonucleotide comprising DNA encoding the human
T cell epitope P2 between stretches of DNA homologous to
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CCCAGGTCCT CTTCCAGTAC ATAAAGGCCA ACTCCAAGTT TATCGGCATC ACCGAGCTCA 60
TCAGCCGCAT CGC 73

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: insertion_seq
 - (B) LOCATION:12..56
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION:/function= "Primer for PCR cloning of DNA encoding TNF-alpha analog"
 - /evidence= EXPERIMENTAL
 - /organism= "Homo sapiens"
 - /standard_name= "Primer "mut2-4""
 - /label= mut2-4
 - /note= "Primer "mut2-4" is a synthetically synthesised 75-mer oligonucleotide comprising DNA encoding the human T cell epitope P2 between stretches of DNA homologous to stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```
AGTCGGTCAC CGAGCTCCGT GATGCCGATG AATTTCGAAT TGGCCTTGAT ATACTGGGGC      60
TTGGCCTCAG CCCCCC                                                    75
```

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: insertion_seq
 - (B) LOCATION:8..52
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION:/function= "Primer for PCR cloning of DNA encoding TNF-alpha analog"
 - /evidence= EXPERIMENTAL
 - /organism= "Homo sapiens"
 - /standard_name= "Primer "mut2-5""
 - /label= mut2-5
 - /note= "Primer "mut2-5" is a synthetically synthesised 75-mer oligonucleotide comprising DNA encoding the human T cell epitope P2 between stretches of DNA homologous to stretches of the human TNF-alpha gene"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GAAGGGTGAC CGACAGTACA TTAAGGCCAA TTCGAAGTTC ATTGGCATCA CTGAGCTGTC 60
TGGGCAGGTC TACTT 75

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: insertion_seq
 - (B) LOCATION:14..58
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut2-7""
/label= mut2-7
/note= "Primer "mut2-7" is a synthetically synthesised
80-mer oligonucleotide comprising DNA encoding the human
T cell epitope P2 between stretches of DNA homologous to
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CACCCATGTG CTCCAGTACA TCAAAGCTAA CTCCAAATTC ATCGGCATCA CCGAACTGGT 60
TAACCTCCTC TCTGCCATCA 80

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

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(ix) FEATURE:

- (A) NAME/KEY: insertion_seq
- (B) LOCATION:10..72
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/function= "Primer for PCR cloning of DNA encoding TNF-alpha analog"
 /evidence= EXPERIMENTAL
 /organism= "Homo sapiens"
 /standard_name= "Primer "mut30-1"
 /label= mut30-1
 /note= "Primer "mut30-1" is a synthetically synthesised 96-mer oligonucleotide comprising DNA encoding the human T cell epitope P30 between stretches of DNA homologous to stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ACCCCGAGTT TCAACAATTT TACCGTAAGC TTTTGGCTCC GTGTACCTAA GGTGTCGGCC 60
 TCGCACCTGG AGCGCCGGGC CAATGCCCTC CTGGCC 96

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: insertion_seq
- (B) LOCATION:12..74
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/function= "Primer for PCR cloning of DNA encoding TNF-alpha analog"
 /evidence= EXPERIMENTAL
 /organism= "Homo sapiens"
 /standard_name= "Primer "mut30-2"
 /label= mut30-2
 /note= "Primer "mut30-2" is a synthetically synthesised 100-mer oligonucleotide comprising DNA encoding human T cell epitope P30 between stretches of DNA homologous to stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TCCTGGCCAA TTTCAACAAC TTCACAGTTA GCTTCTGGTT GAGGGTACCA AAGGTCTCGG 60
 CCAGCCACCT CGAGCAGGTC CTCTTCAAGG GCCAAGGCTG 100

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(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: insertion_seq
 - (B) LOCATION:12..74
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut30-3"
/label= mut30-3
/note= "Primer "mut30-3" is a synthetically synthesised
100-mer oligonucleotide comprising DNA encoding human T
cell epitope P30 between stretches of DNA homologous to
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

CCCAGGTCCT CTTCAACAAC TTTACCGTCT CTTTCTGGCT TCGGGTACCC AAGGTCAGCG      60
CTAGCCACCT CGAGGTCTCC TACCAGACCA AGGTCAACCT                               100

```

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: insertion_seq
 - (B) LOCATION:15..77
 - (C) IDENTIFICATION METHOD: experimental

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(D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut30-4""
/label= mut30-4
/note= "Primer "mut30-4" is a synthetically synthesised
100-mer oligonucleotide comprising DNA encoding human T
cell epitope P30 between stretches of DNA homologous to
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```
AGTCGGTCAC CCTTCTCCAG GTGGGAAGCG CTTACCTTAG GGACGCGCAA CCAGAAGGAC      60
ACGGTGAAAT TATTAAATGG GGTCTCCCTC TGGCAGGGGC                          100
```

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:
(A) NAME/KEY: insertion_seq
(B) LOCATION:14..76
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut30-5""
/label= mut30-5
/note= "Primer "mut30-5" is a synthetically synthesised
100-mer oligonucleotide comprising DNA encoding human T
cell epitope P30 between stretches of DNA homologous to
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```
GAAGGGTGAC CGATTCAACA ATTTACCGT AAGCTTCTGG CTTGCGGTCC CTAAGGTGTC      60
TGCGTCGCAC CTCGAAGGGA TCATTGCCCT CTAGAGTCGA                          100
```

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION:1..25
 (D) OTHER INFORMATION:/label= Pep2-1
 /note= "Pep2-1 is a synthetically prepared truncated form
 of a TNF-alpha analog comprising the human T cell epitope
 P2 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Ser	Arg	Thr	Pro	Ser	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly
1				5				10						15	
Ile	Thr	Glu	Leu	Gln	Leu	Gln	Trp	Leu							
			20				25								

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION:1..25
 (D) OTHER INFORMATION:/label= Pep2-3
 /note= "Pep2-3 is a synthetically prepared truncated form
 of a TNF-alpha analog comprising the human T cell epitope
 P2 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Ser	Gln	Val	Leu	Phe	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly
1				5				10						15	
Ile	Thr	Glu	Leu	Ile	Ser	Arg	Ile	Ala							
			20				25								

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(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION:1..25
 - (D) OTHER INFORMATION:/label= Pep2-4
 /note= "Pep2-4 is a synthetically prepared truncated form
 of a TNF-alpha analog comprising the human T cell epitope
 P2 and flanking portions of human TNF-alpha"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Ala	Glu	Ala	Lys	Pro	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	
1				5				10						15		
Ile	Thr	Glu	Leu	Gly	Asp	Arg	Leu	Ser								
			20				25									

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION:1..25
 - (D) OTHER INFORMATION:/label= Pep2-5
 /note= "Pep2-5 is a synthetically prepared truncated form
 of a TNF-alpha analog comprising the human T cell epitope
 P2 and flanking portions of human TNF-alpha"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Glu	Lys	Gly	Asp	Arg	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	
1				5				10						15		

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Ile Thr Glu Leu Ser Gly Gln Val Tyr
20 25

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION:1..31
 - (D) OTHER INFORMATION:/label= Pep30-1
/note= "Pep30-1 is a synthetically prepared truncated form of a TNF-alpha analog comprising human T cell epitope P30 and flanking portions of human TNF-alpha"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ser	Arg	Thr	Pro	Ser	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg
1				5				10						15	
Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Arg	Arg	Ala	Asn	Ala	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION:1..31
 - (D) OTHER INFORMATION:/label= Pep30-2
/note= "Pep30-2 is a synthetically prepared truncated form of a TNF-alpha analog comprising the human T cell epitope P30 and flanking portions of human TNF-alpha"

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Ala Leu Leu Ala Asn Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
1 5 10 15

Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Val Leu Phe Lys
20 25 30

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION:1..31
(D) OTHER INFORMATION:/label= Pep30-3
/note= "Pep30-3 is a synthetically prepared truncated form of a TNF-alpha analog comprising the human T cell epitope P30 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Tyr	Ser	Gln	Val	Leu	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg
1				5					10					15	
Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Val	Ser	Tyr	Gln	Thr	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- ```
(A) NAME/KEY: Peptide
(B) LOCATION:1..31
```

(D) OTHER INFORMATION:/label= Pep30-4  
 /note= "Pep30-4 is a synthetically prepared truncated form of a TNF-alpha analog comprising the human T cell epitope P30 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Arg | Glu | Thr | Pro | Phe | Asn | Asn | Phe | Thr | Val | Ser | Phe | Trp | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Pro | Lys | Val | Ser | Ala | Ser | His | Leu | Glu | Lys | Gly | Asp | Arg | Leu |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION:1..31  
 (D) OTHER INFORMATION:/label= Pep30-5  
 /note= "Pep30-5 is a synthetically prepared truncated form of a TNF-alpha analog comprising the human T cell epitope P30 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Lys | Gly | Asp | Arg | Phe | Asn | Asn | Phe | Thr | Val | Ser | Phe | Trp | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Pro | Lys | Val | Ser | Ala | Ser | His | Leu | Glu | Gly | Ile | Ile | Ala | Leu |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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